

insularis Emmel & Emmel (Nymphalidae). The former is polyphagous, and I collected its larvae on *Achillea* and *Erigeron* on Santa Rosa. The butterfly is a specialist on Scrophulariaceae, and I found the young larvae on *Castilleja exserta* [= *Orthocarpus purpurascens*], which is a likely host of *C. longana*.

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EFFECTS OF GENE-ENVIRONMENT INTERACTION ON SILK YIELD IN *ANTHRAEA MYLITTA* (SATURNIIDAE)

Additional key words: tasar silk moth, absolute silk yield, *Terminalia arjuna*, stability.

Antheraea mylitta (Drury) is a saturniid moth of considerable commercial value used for production of tasar silk. Because interactions between genotype and environment may exert significant influence over specific life history features (Falconer 1952, Dickerson 1962, Hanson 1964, Breese 1969), it is likely that silk yield and yield contributing traits in different strains of *A. mylitta* are influenced by seasonal and/or environmental factors (Jolly et al. 1979). In an effort to understand features that may contribute to the maximization of silk production, we conducted rearing experiments to measure the interaction between genotype and environment for silk yield and to screen stable genotypes of *A. mylitta* for use in breeding programs to enhance silk yield.

We investigated eight diverse genetic strains of *A. mylitta*: Nagri₁, Nagri₂, Nagri₃, Sukli, Raily, Sukinda, Laris (P), and Palma. The genotype lines were obtained from the germplasm bank of the Central Tasar Research and Training Institute, Ranchi, Bahir, India. We reared the eight genotypes through two generations in July–August and October–November of 1988. The two generations mature under different environmental conditions: the July–August brood occurring during the rainy season, and the October–November brood occurring during the dry season. Larvae were reared on individual plants

TABLE 1. Analysis of variance (ANOVA) for silk yield and related parameters in *Bombyx mori* as a function of genotype and environment. All parameters in the table are significant at $P < 0.01$.

Source	Mean sums of squares							
	Absolute silk yield	Fecundity	Larval weight	Larval span	E.R.R.%	Cocoon weight	Shell weight	Shell ratio
G (genotype)	9586.55	12288.29	28.20	9.30	248.93	17.24	0.28	3.76
E (environment)	83665.97	48260.00	353.27	105.02	737.35	174.57	22.62	533.27
G x E interaction	5663.00	5637.23	21.61	7.59	615.21	2.89	0.14	3.50

of *Terminalia arjuna* Bedd. (Combretaceae) situated in rows, with each plant separated by at least 2 m. Experimental design of the rearings followed a randomized block strategy during both generations, with three replicates of each genotype, 300 larvae per replication. Absolute silk yield was estimated based on shell weight of all the cocoons harvested from each replication. Gene-environment interaction was calculated following the methodology proposed by Plaisted and Peterson (1959). Analysis of variance (ANOVA) was calculated by pooling absolute silk yield of the two seasons.

Table 1 indicates that there were significant differences among genotypes (G), environments (E), and in the gene-environment interaction, suggesting that genotypes interact considerably with environmental conditions to produce different silk yields. Mean absolute silk yield for the two generations and within generation type variance (δ^2_{VL} or stability) are illustrated in Table 2. Mean absolute silk yield ranged from 25.07 g to 147.78 g in the first generation, while that of the second generation ranged from 67.08 g to 259.73 g, illustrating a marked between generation difference. Absolute silk yield was found to be much higher in all genotypes during the second generation, corroborating the findings of Jolly et al. (1979).

As illustrated in Table 2, the genotypes in order of increasing absolute silk yield in the first generation were Palma (25.07 g), Laria (49.49 g), Sukinda (61.46 g), Raily (82.65 g), Nagri₁ (96.70 g), Sukli (98.98 g), Nagri₂ (100.64 g), and Nagri₃ (147.78 g). In the second generation, absolute silk yield (from least to greatest) was achieved by Laria, Nagri₃, Palma, Sukinda, Raily, Sukli, Nagri₂, and Nagri₁.

The estimate of genotype x generation variance exhibited a wide range from 792.96 to 4280.26 (Table 2). The greatest between-generation variability was demonstrated by Nagri₃ followed by Palma, Nagri₂, and Nagri₁. The least between-generation variability was demonstrated by Raily, followed by Sukli and Sukinda. These results suggest that greater stability in silk yield (between generations) could be obtained from Raily. Hence, this genotype would respond better to between-generation differences because of the lesser influence of environment on its absolute silk yield.

TABLE 2. Mean absolute silk yield and stability for eight genotypes of *Bombyx mori* reared in different environments.

Genotypes	Absolute silk yield in environment		G x E interaction
	Rainy season	Dry season	
Nagri ₁	96.70	259.73	2704.48
Nagri ₂	100.64	234.91	2819.07
Nagri ₃	147.78	123.63	4280.26
Sukli	96.98	181.01	952.31
Raily	82.65	157.58	792.96
Sukinda	61.46	156.66	991.73
Laria (P)	49.49	67.08	2190.97
Palma	25.07	148.01	3585.83

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DISTRIBUTION OF A NORTHERN FAUNA OF NOCTUIDAE IN THE MOUNTAINS OF OREGON

Additional key words: endemism, non-target species, biogeography.

Although the Oregon butterfly fauna has been well studied (Dornfeld 1980), comparatively little was known about the Oregon moth fauna until about 1960. During the past 30 years, extensive collecting has been conducted in the state, most notably by Stanley G. Jewett, Jr., C. William Nelson, James H. Baker, Elmer L. Griepentrog, Victor B. McHenry, Kenneth J. Goeden, and Jeffrey C. Miller. From 1992 through 1995, the U. S. Forest Service also conducted extensive blacklight (UV) trap sampling in the Cascade Range and the Blue Mountains to assess the impacts on nontarget Lepidoptera of *Bacillus thuringiensis* subsp. *kurstaki* sprays for suppression of outbreaks of western spruce budworm (*Choristoneura occidentalis* Freeman: Tortricidae) (see Grimble et al. 1992 for details of the sampling protocols in these studies).

Various components of this moth fauna show biogeographic connections with the northern Pacific Coast, California, the Great Basin, and the northern Rocky Mountains. In this paper, we report on a northern fauna of Noctuidae that is transcontinental across Canada from Quebec to British Columbia, extending southward through the Appalachians to North Carolina, the Rocky Mountains, and the mountains of Oregon. The fauna has been enumerated by Rockburne and Lafontaine (1976), Prentice (1962) and from a survey of museum records. Only those species typical of northern hardwood-conifer forests, meadows, or wetlands are included in this study; ubiquitous and/or migratory species throughout most of North America, such as *Heliothis zea* (Boddie) and *Peridroma saucia* (Hbn.), are excluded from consideration.

This northern noctuid fauna is largely confined to three mountainous regions of Oregon; the northern Coast Range, the Cascade Range, and the Blue Mountains. The northern Coast Range consists of low mountains 300–600 m in elevation, with a few higher peaks to 900 m, extending from Clatsop County to coastal Lane County. The Cascade Range extends from Multnomah and Wasco Counties south to Jackson and Klamath Counties. The lower Cascade foothills of the western slope extend from 150–1500 m, whereas the high Cascades are 1200–2100 m in elevation, with high volcanic peaks over 3000 m. The Blue Mountains extend from Crook County northeast to Wallowa County,